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<110> Bougueleret, Lydie

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AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.

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Thr Val Gly Thr Asp Val Ser Ala Lys Tyr Arg Gly Ala Phe Cys Glu
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Ala Lys Ile Lys Thr Ala Lys Arg Leu Val Lys Val Lys Val Thr Phe
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aga cat gat tct tca aca gtg gaa gtt cag gat gac cac ata aag ggc      615
Arg His Asp Ser Ser Thr Val Glu Val Gln Asp Asp His Ile Lys Gly
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Pro Leu Lys Val Gly Ala Ile Val Glu Val Lys Asn Leu Asp Gly Ala
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tat cag gaa gct gtt atc aat aaa cta aca gat gcg agt tgg tac act      711
Tyr Gln Glu Ala Val Ile Asn Lys Leu Thr Asp Ala Ser Trp Tyr Thr
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Val Val Phe Asp Asp Gly Asp Glu Lys Thr Leu Arg Arg Ser Ser Leu
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Cys Leu Lys Gly Glu Arg His Phe Ala Glu Ser Glu Thr Leu Asp Gln
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ctc cca ctc acc aac cct gag cat ttt ggc act cca gtc ata gga aag      855
Leu Pro Leu Thr Asn Pro Glu His Phe Gly Thr Pro Val Ile Gly Lys
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Lys Thr Asn Arg Gly Arg Arg Ser Asn His Ile Pro Glu Glu Glu Ser
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Lys	Lys	Ala	Leu	Trp	Phe	Pro	Ala	Leu	Val	Val	Cys	Pro	Asp	Cys	Ser		
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aaa	caa	gtc	tac	caa	gat	ctt	gga	atc	cct	gtc	tta	aat	tca	gct	gca		1575
Lys	Gln	Val	Tyr	Gln	Asp	Leu	Gly	Ile	Pro	Val	Leu	Asn	Ser	Ala	Ala		
		365					370				375						
gga	tac	aat	ggt	aaa	tgt	gct	tat	aaa	aaa	tac	tta	tat	ggg	ttt	gag		1623
Gly	Tyr	Asn	Val	Lys	Cys	Ala	Tyr	Lys	Lys	Tyr	Leu	Tyr	Gly	Phe	Glu		
		380			385					390							
gag	tac	tgt	aga	tca	gcc	aac	att	gaa	ttt	cag	atg	gca	ttg	cca	gag		1671
Glu	Tyr	Cys	Arg	Ser	Ala	Asn	Ile	Glu	Phe	Gln	Met	Ala	Leu	Pro	Glu		
		395			400				405					410			
aaa	ggt	ggt	aac	aag	caa	tgt	aag	gag	tgt	gaa	aat	gta	aaa	gaa	ata		1719
Lys	Val	Val	Asn	Lys	Gln	Cys	Lys	Glu	Cys	Glu	Asn	Val	Lys	Glu	Ile		
			415					420					425				
aaa	ggt	aag	gag	gaa	aat	gaa	aca	gag	atc	aaa	gaa	ata	aag	atg	gag		1767
Lys	Val	Lys	Glu	Glu	Asn	Glu	Thr	Glu	Ile	Lys	Glu	Ile	Lys	Met	Glu		
		430					435				440						
gag	gag	agg	aat	ata	ata	cca	aga	gaa	gaa	aag	cct	att	gag	gat	gaa		1815
Glu	Glu	Arg	Asn	Ile	Ile	Pro	Arg	Glu	Glu	Lys	Pro	Ile	Glu	Asp	Glu		
		445				450					455						
att	gaa	aga	aaa	gaa	aat	att	aag	ccc	tct	ctg	gga	agt	aaa	aag	aat		1863
Ile	Glu	Arg	Lys	Glu	Asn	Ile	Lys	Pro	Ser	Leu	Gly	Ser	Lys	Lys	Asn		

460	465	470	
tta tta gaa tct ata cct aca cat tct gat cag gaa aaa gaa gtt aac			1911
Leu Leu Glu Ser Ile Pro Thr His Ser Asp Gln Glu Lys Glu Val Asn			
475	480	485	490
att aaa aaa cca gaa gac aat gaa aat ctg gay gac aaa gat gat gac			1959
Ile Lys Lys Pro Glu Asp Asn Glu Asn Leu Asp Asp Lys Asp Asp Asp			
495	500	505	
aca act agg gta gat gaa tcc ctc aac ata aag gta gaa gct gag gaa			2007
Thr Thr Arg Val Asp Glu Ser Leu Asn Ile Lys Val Glu Ala Glu Glu			
510	515	520	
gaa aaa gca aaa tct gga gat gaa acg aat aaa gaa gaa gat gaa gat			2055
Glu Lys Ala Lys Ser Gly Asp Glu Thr Asn Lys Glu Glu Asp Glu Asp			
525	530	535	
gat gaa gaa gca gaa gag gag gag gag gag gaa gaa gaa gaa gag gat			2103
Asp Glu Glu Ala Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp			
540	545	550	
gaa gat gat gat gac aac aat gag gaa gag gag ttt gag tgc tat cca			2151
Glu Asp Asp Asp Asp Asn Asn Glu Glu Glu Glu Phe Glu Cys Tyr Pro			
555	560	565	570
cca ggc atg aaa gtc caa gtg cgg tat gga cga ggg aaa aat caa aaa			2199
Pro Gly Met Lys Val Gln Val Arg Tyr Gly Arg Gly Lys Asn Gln Lys			
575	580	585	
atg tat gaa gct agt att aaa gat tct gat gtt gaa ggt gga gag gtc			2247
Met Tyr Glu Ala Ser Ile Lys Asp Ser Asp Val Glu Gly Gly Glu Val			
590	595	600	
ctt tac ttg gtg cat tac tgc gga tgg aat gtg aga tac gat gaa tgg			2295
Leu Tyr Leu Val His Tyr Cys Gly Trp Asn Val Arg Tyr Asp Glu Trp			
605	610	615	
att aaa gca gat aaa ata gta aga cct gct gat aaa aat gtg cca aag			2343
Ile Lys Ala Asp Lys Ile Val Arg Pro Ala Asp Lys Asn Val Pro Lys			
620	625	630	
ata aaa cat cgg aag aaa ata aag aat aaa tta gac aaa gaa aaa gac			2391
Ile Lys His Arg Lys Lys Ile Lys Asn Lys Leu Asp Lys Glu Lys Asp			
635	640	645	650
aaa gat gaa aaa tac tct cca aaa aac tgt aaa ctt cgg cgc ttg tcc			2439
Lys Asp Glu Lys Tyr Ser Pro Lys Asn Cys Lys Leu Arg Arg Leu Ser			
655	660	665	
aaa cca cca ttt cag aca aat cca tct cct gaa atg gta tcc aaa ctg			2487
Lys Pro Pro Phe Gln Thr Asn Pro Ser Pro Glu Met Val Ser Lys Leu			
670	675	680	
gat ctc act gat gcc aaa aac tct gat act gct cat att aag tcc ata			2535
Asp Leu Thr Asp Ala Lys Asn Ser Asp Thr Ala His Ile Lys Ser Ile			
685	690	695	
gaa att act tcg atc ctt aat gga ctt caa gct tct gaa agt tct gct			2583
Glu Ile Thr Ser Ile Leu Asn Gly Leu Gln Ala Ser Glu Ser Ser Ala			
700	705	710	
gaa gac agt gag cag gaa gat gag aga ggt gct caa gac atg gat aat			2631
Glu Asp Ser Glu Gln Glu Asp Glu Arg Gly Ala Gln Asp Met Asp Asn			
715	720	725	730
aat ggc aaa gag gaa tct aag att gat cat ttg acc aac aac aga aat			2679
Asn Gly Lys Glu Glu Ser Lys Ile Asp His Leu Thr Asn Asn Arg Asn			
735	740	745	
gat ctt att tca aag gag gaa cag aac agt tca tct ttg cta gaa gaa			2727
Asp Leu Ile Ser Lys Glu Glu Gln Asn Ser Ser Ser Leu Leu Glu Glu			
750	755	760	
aac aaa gtt cat gca gat ttg gta ata tcc aaa cca gtg tca aaa tct			2775
Asn Lys Val His Ala Asp Leu Val Ile Ser Lys Pro Val Ser Lys Ser			

cca gaa aga tta agg aaa gat	765	770	775	2823
Pro Glu Arg Leu Arg Lys Asp		Ile Glu Val Leu Ser	Glu Asp Thr Asp	
780		785	790	
tat gaa gaa gat gaa gtc aca		aaa aag aga aag gat gtc	aag aag gac	2871
Tyr Glu Glu Asp Glu Val Thr		Lys Lys Arg Lys Asp Val	Lys Lys Asp	
795		800	805	810
aca aca gat aaa tct tca aaa		cca caa ata aaa cgt ggt	aaa aga agg	2919
Thr Thr Asp Lys Ser Ser Lys		Pro Gln Ile Lys Arg Gly	Lys Arg Arg	
	815	820	825	
tat tgc aat aca gaa gag tgt		cta aaa act gga tca cct	ggc aaa aag	2967
Tyr Cys Asn Thr Glu Glu Cys		Leu Lys Thr Gly Ser Pro	Gly Lys Lys	
	830	835	840	
gaa gag aag gcc aag aac aaa		gaa tca ctt tgc atg gaa	aac agt agc	3015
Glu Glu Lys Ala Lys Asn Lys		Glu Ser Leu Cys Met Glu	Asn Ser Ser	
	845	850	855	
aac agc tct tca gat gaa gat		gaa gaa gaa aca aaa gca	aag atg aca	3063
Asn Ser Ser Ser Asp Glu Asp		Glu Glu Glu Thr Lys Ala	Lys Met Thr	
	860	865	870	
cca act aag aaa tac aat ggt		ttg gag gaa aaa aga aaa	tct cta cgg	3111
Pro Thr Lys Lys Tyr Asn Gly		Leu Glu Glu Lys Arg Lys	Ser Leu Arg	
	875	880	885	890
aca act ggt ttc tat tca gga		ttt tca gaa gtg gca gaa	aaa agg att	3159
Thr Thr Gly Phe Tyr Ser Gly		Phe Ser Glu Val Ala Glu	Lys Arg Ile	
	895	900	905	
aaa ctt tta aat aac tct gat		gaa aga ctt caa aac agc	agg gcc aaa	3207
Lys Leu Leu Asn Asn Ser Asp		Glu Arg Leu Gln Asn Ser	Arg Ala Lys	
	910	915	920	
gat cga aaa gat gtc tgg tca		agt att cag gga cag tgg	cct aaa aaa	3255
Asp Arg Lys Asp Val Trp Ser		Ser Ile Gln Gly Gln Trp	Pro Lys Lys	
	925	930	935	
acg ctg aaa gag ctt ttt tca		gac tct gat act gag gct	gca gct tcc	3303
Thr Leu Lys Glu Leu Phe Ser		Asp Ser Asp Thr Glu Ala	Ala Ala Ser	
	940	945	950	
cca ccg cat cct gcc cca gag		gag grg gtg gca gag gag	tca mtg cag	3351
Pro Pro His Pro Ala Pro Glu		Glu Glu Xaa Val Ala Glu	Glu Ser Xaa Gln	
	955	960	965	970
act gtg gct gaa gag gag agt		tgt tca ccc agt gta gaa	cta gaa aaa	3399
Thr Val Ala Glu Glu Ser Cys		Ser Pro Ser Val Glu Leu	Glu Lys	
	975	980	985	
cca cct cca gtc aat gtc gat		agt aaa ccc att gaa gaa	aaa aca gta	3447
Pro Pro Pro Val Asn Val Asp		Ser Lys Pro Ile Glu Glu	Lys Thr Val	
	990	995	1000	
gag gtc aat gac aga aaa gca		gaa ttt cca agt agt ggc	agt aat tca	3495
Glu Val Asn Asp Arg Lys Ala		Glu Phe Pro Ser Ser Gly	Ser Asn Ser	
	1005	1010	1015	
gtg cta aat acc cct cct act		aca cct gaa tcg cct tca	tca gtc act	3543
Val Leu Asn Thr Pro Pro Thr		Thr Thr Pro Glu Ser Pro	Ser Ser Val Thr	
	1020	1025	1030	
gta aca gaa ggc agc cgg cag		cag tct tct gta aca gta	tca gaa cca	3591
Val Thr Glu Gly Ser Arg Gln		Gln Gln Ser Ser Val Thr	Val Ser Glu Pro	
	1035	1040	1045	1050
ctg gct cca aac caa gaa gag		gtt cga agt atc aag agt	gaa act gat	3639
Leu Ala Pro Asn Gln Glu Glu		Val Arg Ser Ile Lys Ser	Glu Thr Asp	
	1055	1060	1065	
agc aca att gag gtg gat agt		gtt gct ggg gag ctc caa	gac ctc cag	3687
Ser Thr Ile Glu Val Asp Ser		Val Ala Gly Glu Leu Gln	Asp Leu Gln	

tct gaa ggg aat agc tcg cca gca ggt ttt gat gcc agt gtg agc tca	1070	1075	1080	3735
Ser Glu Gly Asn Ser Ser Pro Ala Gly Phe Asp Ala Ser Val Ser Ser				
agc agt agt aat cag cca gaa cca gaa cat cct gaa aaa gcc tgt aca	1085	1090	1095	3783
Ser Ser Ser Asn Gln Pro Glu Pro Glu His Pro Glu Lys Ala Cys Thr				
ggt cag aaa aga gtg aaa gat gct cag gga gga agt tca tca aaa	1100	1105	1110	3831
Gly Gln Lys Arg Val Lys Asp Ala Gln Gly Gly Ser Ser Ser Lys				
aag cag aaa aga agc cat aaa gca aca gtg gta aac aac aaa aag aag	1115	1120	1125	3879
Lys Gln Lys Arg Ser His Lys Ala Thr Val Val Asn Asn Lys Lys Lys				
gga aaa ggc aca aat agt agt gat agt gaa gaa ctt tca gct ggt gaa	1135	1140	1145	3927
Gly Lys Gly Thr Asn Ser Ser Asp Ser Glu Glu Leu Ser Ala Gly Glu				
agt ata act aag agt cag cca gtc aaa tca gtt tcc act gga atg aag	1150	1155	1160	3975
Ser Ile Thr Lys Ser Gln Pro Val Lys Ser Val Ser Thr Gly Met Lys				
tct cat agt acc aaa tct ccc gca agg acg cag tct cca gga aaa tgt	1165	1170	1175	4023
Ser His Ser Thr Lys Ser Pro Ala Arg Thr Gln Ser Pro Gly Lys Cys				
gga aag aat ggt gat aag gat cct gat ctc aag gaa ccc agt aat cga	1180	1185	1190	4071
Gly Lys Asn Gly Asp Lys Asp Pro Asp Leu Lys Glu Pro Ser Asn Arg				
tta ccc aaa gtt tac aaa tgg agt ttt cag atg tcg gac ctg gaa aat	1195	1200	1205	4119
Leu Pro Lys Val Tyr Lys Trp Ser Phe Gln Met Ser Asp Leu Glu Asn				
atg aca agt gcc gaa cgc atc aca att ctt caa gaa aaa ctt caa gaa	1215	1220	1225	4167
Met Thr Ser Ala Glu Arg Ile Thr Ile Leu Gln Glu Lys Leu Gln Glu				
atc aga aaa cat tat ctg tca tta aaa tct gaa gta gct tcc att gat	1230	1235	1240	4215
Ile Arg Lys His Tyr Leu Ser Leu Lys Ser Glu Val Ala Ser Ile Asp				
cgg agg aga aag cgt tta aag aag aaa gag aga gaa agt gct gct aca	1245	1250	1255	4263
Arg Arg Arg Lys Arg Leu Lys Lys Lys Glu Arg Glu Ser Ala Ala Thr				
tcc tca tcc tcc tct tca cct tca tcc agt tcc ata aca gct gct gtt	1260	1265	1270	4311
Ser Ser Ser Ser Ser Ser Pro Ser Ser Ser Ser Ile Thr Ala Ala Val				
atg tta act tta gct gaa ccg tca atg tcc agc gca tca caa aat gga	1275	1280	1285	4359
Met Leu Thr Leu Ala Glu Pro Ser Met Ser Ser Ala Ser Gln Asn Gly				
atg tca gtt gag tgc agg tga cagcaggact tgctaaagca ctttgcactt	1295	1300	1305	4410
Met Ser Val Glu Cys Arg *				
aatggctgtt gagggccact ttttttttat actgcacagt ggcacaaaaa aatatcagac	1310			4470
aagcactatt ttatatitaa aaattgtttc ttgacaagct gacttggcac ttaagtgcac				4530
ttttttatga agaaaaagta caatgaactg cttttcctca agcaataatt gkttccaact				4590
tgtctgggaa ttgtgtgtct ggtaactgga aggccttcca ctgtggcaaa tggaggcttt				4650
tcactgcctg tagagacaat acagtaagca tagttaagggt gtgggtcaga acatgttaag				4710
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gaattataac	agttatat	ttgtgttttc	ttgtaaatgt	ttcttttccc	ttaaatacag	5250
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tctgttctgt	ttggcacttg	tatttaattc	ttcacctttg	taagacattt	gtatattgtg	5550
gatgtgttca	ttcaagctat	ttaatatctg	gcactgttaa	tacacagtac	tttattgtac	5610
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 <212> DNA
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cctctggagg	gcagcgcgat	tgggggcccc	gacctccagt	ccgggggggga	tttttcgctg	180
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gcgaggagg	gaggagccgg	agcctctgcc	tcagcagccg	ctggaccgcc	cgcccttctt	300
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cgtgccaggg	tcagatctcg	cctccgagga	ag			392

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 <211> 55
 <212> DNA
 <213> Homo sapiens

<400> 6						
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 <212> DNA
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 <211> 66
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 <213> Homo sapiens

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<210> 9
 <211> 91
 <212> DNA
 <213> Homo sapiens

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 aaactaacag atgcgagttg gtacactgta g 91

 <210> 10
 <211> 80
 <212> DNA
 <213> Homo sapiens

 <400> 10
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 ggcattttgc tgaaagtga 80

 <210> 11
 <211> 92
 <212> DNA
 <213> Homo sapiens

 <400> 11
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 aaaacaaata gaggaagaag atctaatac at 92

 <210> 12
 <211> 139
 <212> DNA
 <213> Homo sapiens

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 actgtggttt cctgcattg 139

 <210> 13
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 <212> DNA
 <213> Homo sapiens

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 tctttcaaag atggaaaatt 80

 <210> 14
 <211> 77
 <212> DNA
 <213> Homo sapiens

 <400> 14
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 tgctgtttta aagcaag 77

 <210> 15
 <211> 155

<212> DNA

<213> Homo sapiens

<400> 15

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aaaaaagaaa	ggaggataat	agcagtgaag	aagag			155

<210> 16

<211> 73

<212> DNA

<213> Homo sapiens

<400> 16

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<210> 17

<211> 95

<212> DNA

<213> Homo sapiens

<400> 17

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<210> 18

<211> 98

<212> DNA

<213> Homo sapiens

<400> 18

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<210> 19

<211> 244

<212> DNA

<213> Homo sapiens

<400> 19

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taaggaggaa	aatgaaacag	agatcaaaga	aataaagatg	gaggaggaga	ggaatataat	180
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<210> 20

<211> 176

<212> DNA

<213> Homo sapiens

<400> 20

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<210> 21
 <211> 258
 <212> DNA
 <213> Homo sapiens

<400> 21							
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ggaagaagaa	gaagaggatg	aagatgatga	tgacaacaat	gaggaagagg	agtttgagtg		120
ctatccacca	ggcatgaaa	tccaagtgcg	gtatggacga	gggaaaaatc	aaaaaatgta		180
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ctgcggatgg	aatgtgag						258

<210> 22
 <211> 85
 <212> DNA
 <213> Homo sapiens

<400> 22							
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gataaaacat	cggaagaaaa	taaag					85

<210> 23
 <211> 199
 <212> DNA
 <213> Homo sapiens

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<210> 24
 <211> 1209
 <212> DNA
 <213> Homo sapiens

<400> 24							
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Lys	Arg	Leu	Val	Lys	Val	Lys	Val	Thr	Phe	Arg	His	Asp	Ser	Ser	Thr
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Val	Glu	Val	Gln	Asp	Asp	His	Ile	Lys	Gly	Pro	Leu	Lys	Val	Gly	Ala
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Asp	Glu	Lys	Thr	Leu	Arg	Arg	Ser	Ser	Leu	Cys	Leu	Lys	Gly	Glu	Arg
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His	Phe	Ala	Glu	Ser	Glu	Thr	Leu	Asp	Gln	Leu	Pro	Leu	Thr	Asn	Pro
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Glu	His	Phe	Gly	Thr	Pro	Val	Ile	Gly	Lys	Lys	Thr	Asn	Arg	Gly	Arg
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Arg	Ser	Asn	His	Ile	Pro	Glu	Glu	Glu	Ser	Ser	Ser	Ser	Ser	Ser	Asp

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Val	Cys	Val	Asp	Tyr	Ile	Ser	Leu	Asp	Lys	Lys	Lys	Ala	Leu	Trp	Phe
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Phe	Pro	Glu	Glu	Arg	Glu	Asn	Phe	Leu	Gln	Gln	Leu	Tyr	Lys	Phe	Met
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Glu	Asp	Arg	Gly	Thr	Pro	Ile	Asn	Lys	Arg	Pro	Val	Leu	Gly	Tyr	Arg
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785				790					795						800
Thr	Lys	Lys	Arg	Lys	Asp	Val	Lys	Lys	Asp	Thr	Thr	Asp	Lys	Ser	Ser
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1010						1015					1020				
Thr	Thr	Pro	Glu	Ser	Pro	Ser	Ser	Val	Thr	Val	Thr	Glu	Gly	Ser	Arg
1025				1030					1035						1040
Gln	Gln	Ser	Ser	Val	Thr	Val	Ser	Glu	Pro	Leu	Ala	Pro	Asn	Gln	Glu
				1045					1050					1055	
Glu	Val	Arg	Ser	Ile	Lys	Ser	Glu	Thr	Asp	Ser	Thr	Ile	Glu	Val	Asp

1060	1065	1070
Ser Val Ala Gly Glu Leu Gln Asp	Leu Gln Ser Glu Gly Asn Ser Ser	
1075	1080	1085
Pro Ala Gly Phe Asp Ala Ser Val	Ser Ser Ser Ser Ser Asn Gln Pro	
1090	1095	1100
Glu Pro Glu His Pro Glu Lys Ala Cys Thr	Gly Gln Lys Arg Val Lys	
1105	1110	1115
Asp Ala Gln Gly Gly Ser Ser Ser Lys	Lys Gln Lys Arg Ser His	
1125	1130	1135
Lys Ala Thr Val Val Asn Asn Lys Lys	Lys Gly Lys Gly Thr Asn Ser	
1140	1145	1150
Ser Asp Ser Glu Glu Leu Ser Ala Gly	Glu Ser Ile Thr Lys Ser Gln	
1155	1160	1165
Pro Val Lys Ser Val Ser Thr Gly Met	Lys Ser His Ser Thr Lys Ser	
1170	1175	1180
Pro Ala Arg Thr Gln Ser Pro Gly Lys	Cys Gly Lys Asn Gly Asp Lys	
1185	1190	1195
Asp Pro Asp Leu Lys Glu Pro Ser Asn	Arg Leu Pro Lys Val Tyr Lys	
1205	1210	1215
Trp Ser Phe Gln Met Ser Asp Leu Glu	Asn Met Thr Ser Ala Glu Arg	
1220	1225	1230
Ile Thr Ile Leu Gln Glu Lys Leu Gln	Glu Ile Arg Lys His Tyr Leu	
1235	1240	1245
Ser Leu Lys Ser Glu Val Ala Ser Ile	Asp Arg Arg Arg Lys Arg Leu	
1250	1255	1260
Lys Lys Lys Glu Arg Glu Ser Ala Ala	Thr Ser Ser Ser Ser Ser Ser	
1265	1270	1275
Pro Ser Ser Ser Ser Ile Thr Ala Ala	Val Met Leu Thr Leu Ala Glu	
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39

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49

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<210> 63
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<210> 65
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<220>
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<223> base T ; G in SEQ ID48

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<223> potential microsequencing oligo 5-148-352.mis1

<220>
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<400> 69
tgcttttccct caagcaataa ttgtttccaa cttgtctggg aattgtg

47

<210> 70

<211> 47
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<220>
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<223> polymorphic fragment 99-1437-325, variant version of SEQ ID49

<220>
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<223> base T ; C in SEQ ID49

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<222> 1..23
<223> potential microsequencing oligo 99-1437-325.mis1

<220>
<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-1437-325.mis2

<400> 70
caagagctga catttactgc atattttaatt tgtgccgaac actgaac 47

<210> 71
<211> 47
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<220>
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<222> 1..47
<223> polymorphic fragment 99-1442-224, variant version of SEQ ID50

<220>
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<222> 24
<223> base T ; G in SEQ ID50

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<223> potential microsequencing oligo 99-1442-224.mis1

<220>
<221> primer_bind
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<223> complement potential microsequencing oligo 99-1442-224.mis2

<400> 71
attaatctca gtcataatctt gggttttttt tcttctctta taattaa 47

<210> 72
<211> 19

<212> DNA
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<223> upstream amplification primer for SEQ 30, SEQ 51

<400> 72
aaaagaaaac aaacccagg 19

<210> 73
<211> 19
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<223> upstream amplification primer for SEQ 31, SEQ 52

<400> 73
ataagagttt gggaatacc 19

<210> 74
<211> 18
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<223> upstream amplification primer for SEQ 32, SEQ 53

<400> 74
tggaaggatg taggatgc 18

<210> 75
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<223> upstream amplification primer for SEQ 33, SEQ 54

<400> 75
gctactctgt gtgcaatc 18

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<212> DNA
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<222> 1..20
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 <400> 76
 caaacaataa atgtcagtgg 20

 <210> 77
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 <223> upstream amplification primer for SEQ 36, SEQ 57

 <400> 77
 ggttttgaac agcttagtg 19

 <210> 78
 <211> 18
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 <223> upstream amplification primer for SEQ 37, SEQ 58

 <400> 78
 tcttttgagt ctaggacc 18

 <210> 79
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 <223> upstream amplification primer for SEQ 38, SEQ 59, SEQ 39, SEQ 60, SEQ 40, SEQ 61

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19

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gggcttctta tggtctttc

19

<210> 82
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<400> 82
gcctaaaaaa acgctgaaag

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<210> 83
<211> 19
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<220>
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<223> upstream amplification primer for SEQ 47, SEQ 68

<400> 83
tagtaagttc tgtgacaac

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<210> 84
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<223> upstream amplification primer for SEQ 48, SEQ 69

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18

<210> 85
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<400> 85
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<210> 86
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<211> 19
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<400> 87
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<400> 88
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<210> 89
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<223> downstream amplification primer for SEQ 33, SEQ 54

<400> 90
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<210> 91
<211> 20
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<400> 91
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<210> 92
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<223> downstream amplification primer for SEQ 36, SEQ 57

<400> 92
gctatcaaat tcctcatc 19

<210> 93
<211> 20
<212> DNA
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<220>
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<400> 93
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<210> 94
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<400> 94
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<210> 95
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<210> 96
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<400> 96
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<210> 97
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<400> 97
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<400> 98
gtttttttaa gcaagtagcc 20

<210> 99
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<400> 99
aaagcctcca ttgcccacag 20

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<223> downstream amplification primer for SEQ 49, SEQ 70

<400> 100
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<210> 101
<211> 19
<212> DNA
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<220>
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<223> downstream amplification primer for SEQ 50, SEQ 71

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<210> 102
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<222> 1..19
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<400> 102
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<210> 103
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<220>
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<400> 103
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<210> 104
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<400> 104
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<210> 105
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<400> 105
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<210> 106
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<210> 107
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<400> 107
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<210> 108
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<210> 109
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<210> 110
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<210> 120

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<210> 123
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19

<210> 135

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<210> 136

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18

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